AMENDMENTS TO THE SPECIFICATION

Please amend paragraphs [0049], [0063], and [0120] in the specification as the follows:

[0049] Figure 3 lists a set of atomic structure coordinates for HDAC-2 (SEQ ID NO:5) as derived by X-ray crystallography from a crystal that comprises the protein. The following abbreviations are used in Figure 3: "X, Y, Z" crystallographically define the atomic position of the element measured; "B" is a thermal factor that measures movement of the atom around its atomic center; "Occ" is an occupancy factor that refers to the fraction of the molecules in which each atom occupies the position specified by the coordinates (a value of "1" indicates that each atom has the same conformation, i.e., the same position, in all molecules of the crystal).

[0063] It is also noted that the above sequences of HDAC-2 is also intended to encompass isoforms, mutants and fusion proteins of these sequences. An example of a fusion protein is provided by ~~SEQ. ID No. 3~~ SEQ ID NO:3 which includes a 7 residue C-terminal tag (GHHHHHH) (residues 489-495 of SEQ ID NO:3) that may be used to facilitate purification of the protein.

[0120] It is noted that the sequence of the structure coordinates presented in Figures 3 differ in some regards from the sequence shown in ~~SEQ. ID No. 5~~ SEQ ID NO:5. It is noted structure coordinates are not reported for some residues because the electron density obtained was insufficient to identify the position of these residues. For Figure 3, chain A, structure coordinates for residues 1-~~12~~ 11 and 379-409 (using numbering from ~~SEQ. ID No. 5~~ SEQ ID NO:5) are not reported. For Figure 3, chain B, structure coordinates for residues 1-13 and 379-409 are not reported. For Figure 3, chain C, structure coordinates for residues 1-13 and 379-409 are not reported.